

DGPs Preconference Workshop 2018



Multinomial Processing Tree (MPT) Modeling: Basic Methods and Recent Advances

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5) Advanced features of multiTree

- 5.1) Identifiability checks in multiTree
- 5.2) Statistical Power Analyses
- 5.3) Model selection

5.1) Identifiability checks in multiTree

- Get Jacobian
 - Evaluate at random parameter location
 - Use parameter values from parameter tab
- Repeated analysis
 - Check stability of parameters estimates
- Simulated identifiability
 - Repeated analysis for different random locations in Ω

5.2) Statistical power analysis in multiTree

Traditional Power Analysis (Cohen, 1969, 1972, 1988)

- Under H_1 , the Power-Divergence statistic (S_λ) follows a noncentral chi-square distribution with noncentrality parameter $\gamma_{(\lambda)} = N \cdot \mathbf{w}_{(\lambda)}^2$, where $\mathbf{w}_{(\lambda)}$ denotes the effect size ($\mathbf{w}_{(\lambda)}^2 = S_\lambda(H_1\text{-Parameter}) / N$)
- Effect size conventions
 - $w = .10$ (“small effect“)
 - $w = .30$ (“medium effect“)
 - $w = .50$ (“large effect“)
- Types of power analysis
 - “A priori”: Compute N as a function of w , α , and $1-\beta$
 - “Post hoc”: Compute $1-\beta$ as a function of w , α , and N

Problems of the traditional method

- Problem 1:
 - How does effect size translate into parameter values?
- Problem 2:
 - Same meaning of effect size labels in different models?
- Problem 3:
 - Relative size of groups/conditions is ignored.

Cohen (1988, p. 244)

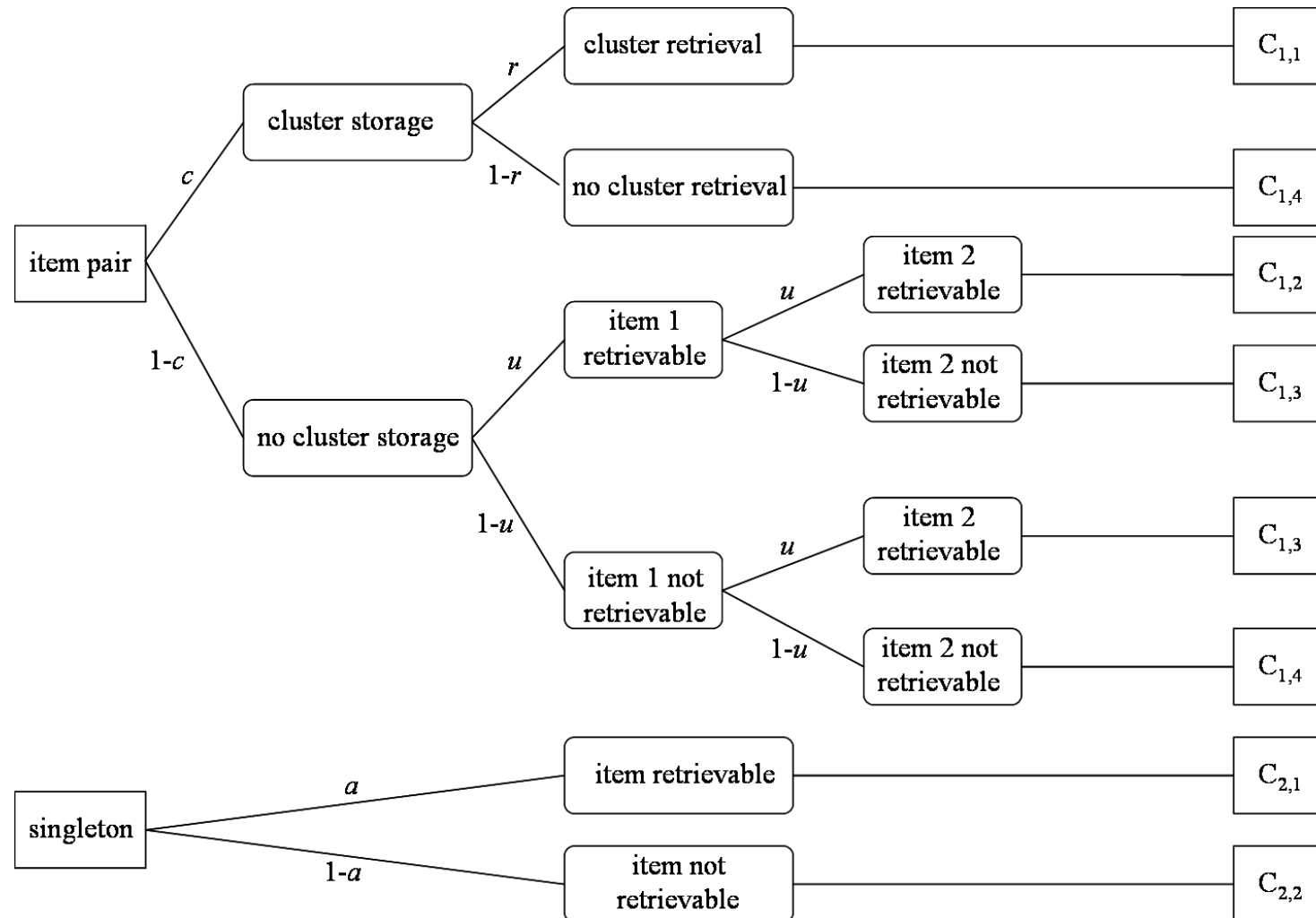
On w effect sizes conventions:

“Their use requires particular caution, since, apart from their possible inaptness in a particular substantive context, what is subjectively the same degree of departure or degree of correlation (...) may yield varying w , and conversely. **The investigator is best advised to use the conventional definitions as a general frame of reference (...) and not to take them too literally.**”

Approach 2: Power as a function of the model parameters under H_1

- 1) Specify your H_0 model
- 2) Specify your H_1 model with all parameter values fixed at „plausible values“
- 3) Choose N_k , $k = 1, \dots, K$, and calculate expected frequencies under H_1
- 4) Fit the H_0 model to the H_1 expected frequencies by minimizing PD^λ for some λ
- 5) Use the minimum PD^λ value as the ncp $\gamma_{(\lambda)}$
- 6) Compute $1-\beta(\pi) = Pr(\chi^2(\gamma_{(\lambda)}), df) \geq c_{(df, \alpha)})$

An example: The storage retrieval model



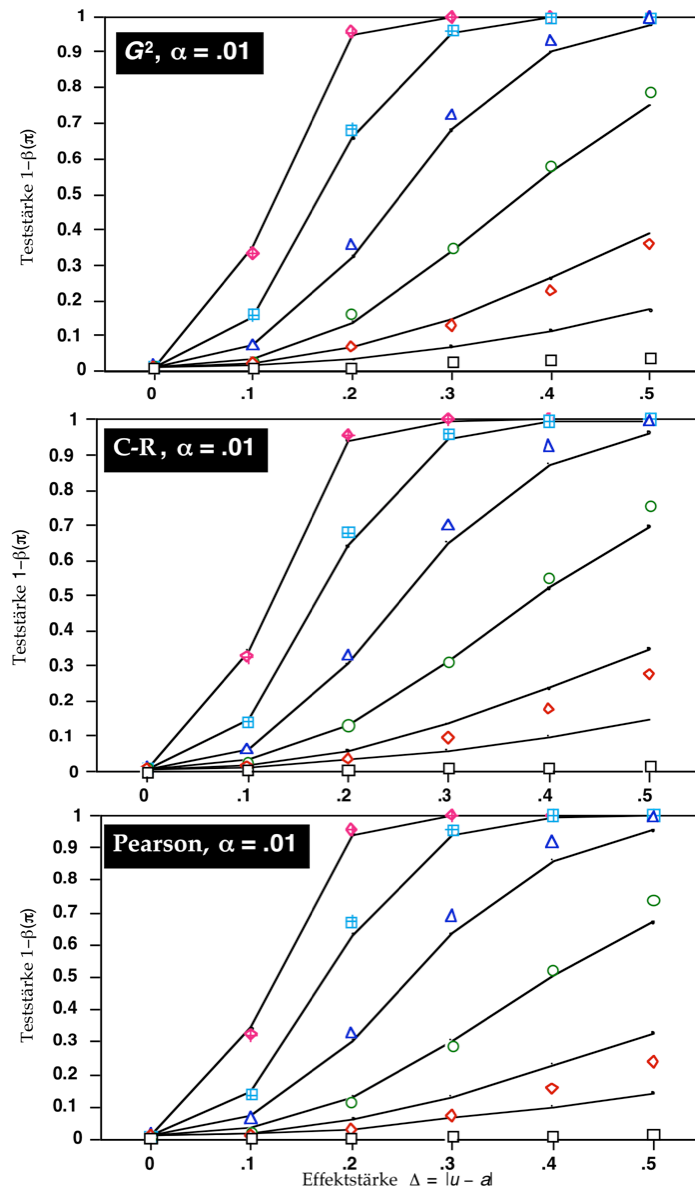
Open questions

- How good are these approximations for joint MPT models?
- How does approximation quality depend on the sample sizes?
- Does the approximation quality depend on the PD^λ test statistic used?
- Does the approximation quality depend on the λ -value used to compute the ncp?

A Monte-Carlo study

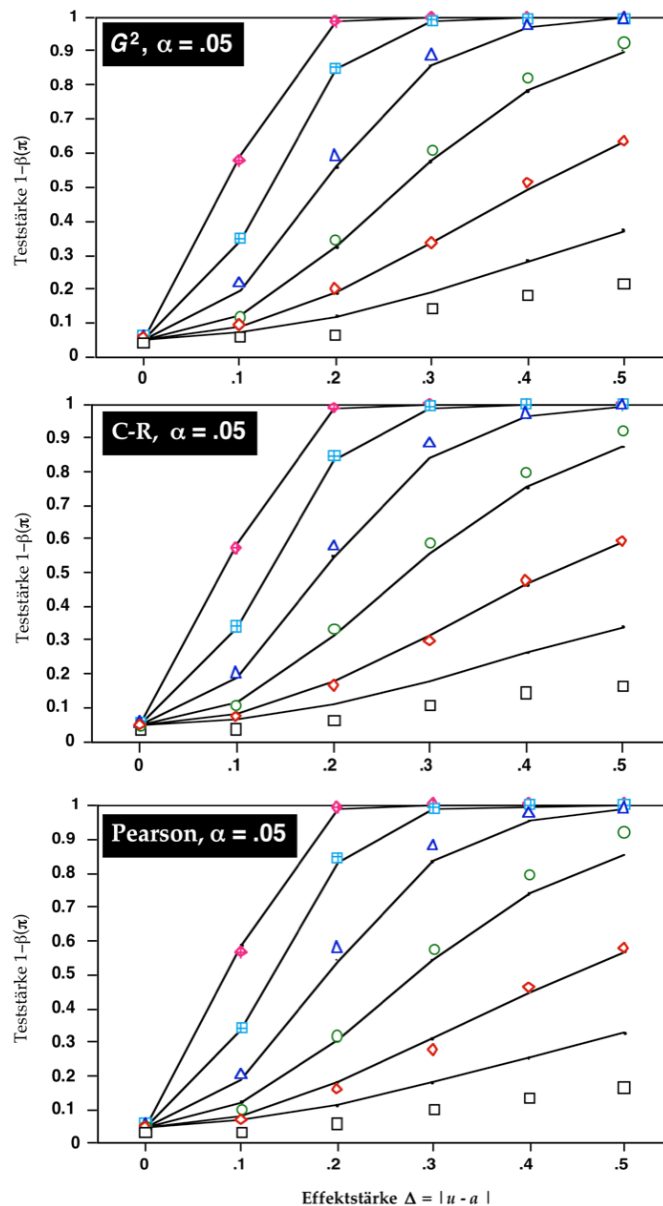
- Storage-retrieval model ($\tau_1 = 2/3$, $\tau_2 = 1/3$)
- H_0 : $u = a$, $df = 4 - 3 = 1$
- H_1 : $c = r = .5$, $u = .5 - \Delta/2$, $a = .5 + \Delta/2$, for
 $\Delta = .00 / .10 / .20 / .30 / .40 / .50$
($w = .00 / .07 / .13 / .19 / .24 / .28$)
- $N = 30 / 60 / 120 / 240 / 480 / 960$
- Type-1 errors $\alpha = .01 / .05 / .10$
- Statistics: G^2 , X^2 , Cressie-Read
- Noncentrality parameter: $\gamma_{(\lambda=0)}$, $\gamma_{(\lambda=1)}$, $\gamma_{(\lambda=2/3)}$
- 1000 Monte Carlo samples per run

Results for $\alpha = .01$



- *Symbols:* Monte-Carlo estimated power for G^2 (top), Cressie-Read (middle), and X^2 (bottom).
- *Black lines:* Approximate power using same λ in $n_{cp} \gamma_{(\lambda)}$ as in PD^λ test statistic
- Sample sizes from top to bottom:
 - $N = 960$
 - $N = 480$
 - $N = 240$
 - $N = 120$
 - $N = 60$
 - $N = 30$

Results for $\alpha = .05$



- *Symbols:* Monte-Carlo estimated power for G^2 (top), Cressie-Read (middle), and X^2 (bottom).
- *Black lines:* Approximate power using same λ in $n_{cp} \gamma_{(\lambda)}$ as in PD^λ test statistic
- Sample sizes from top to bottom:
 - $N = 960$
 - $N = 480$
 - $N = 240$
 - $N = 120$
 - $N = 60$
 - $N = 30$

Absolute differences between Monte-Carlo power and approximate power formula ($\alpha = .05$)

	Test statistic and ncp used					
	G^2 with $\gamma_{(0)}$		$C-R$ with $\gamma_{(2/3)}$		X^2 with $\gamma_{(1)}$	
N	mean	max.	mean	max.	mean	max.
30	.065	.157	.075	.173	.078	.162
60	.007	.019	.010	.020	.015	.032
120	.021	.040	.027	.049	.031	.066
240	.017	.031	.020	.041	.021	.048
480	.004	.011	.005	.010	.006	.014
960	.003	.014	.003	.014	.004	.016
Mean	.020	.045	.023	.051	.026	.056

Conclusions from the Monte-Carlo study

- In our example, the power approximation is acceptable for $N > 50$ and good for $N > 200$
- Use the same λ parameter in the PD^λ statistic and the noncentrality parameter $\gamma(\lambda)$
- Approximation accuracy appears to be worse for $\alpha = .01$ compared to $\alpha = .05$ and $\alpha = .10$
- In general, the effect of λ on approximation accuracy appears to be small.
- However, approximation accuracy is slightly larger for G^2 compared to both the Cressie-Read statistic and Pearson's X^2 .

Power optimization

Problem:

Given a fixed total sample size and a fixed α , is there any way to maximize the power?

Answer:

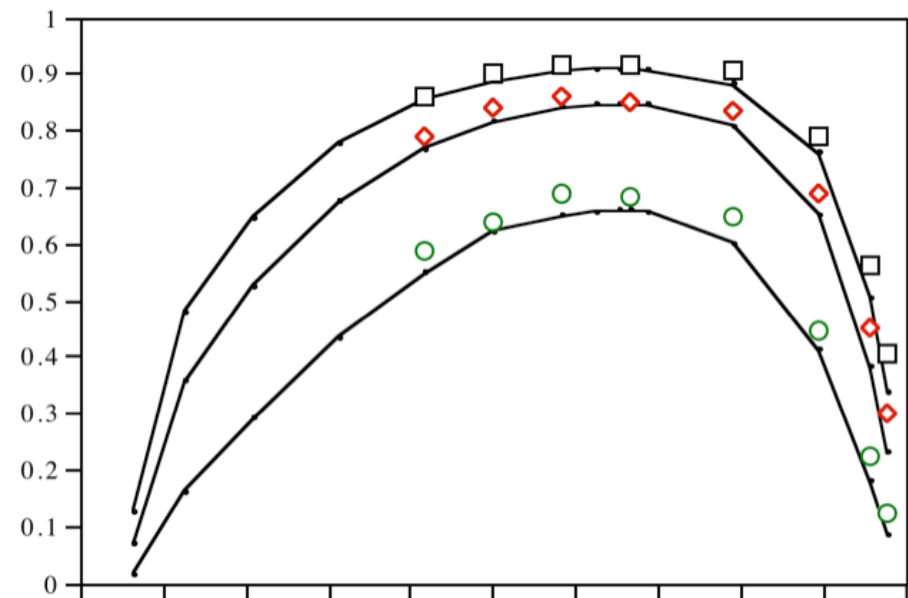
Yes, there are many!

1) λ Optimization

- Asymptotic results (see Read & Cressie, 1988):
 - Pitman efficiency (or Asymptotic Relative Efficiency, A.R.E.) of two different PD^λ statistics is always 1.
 - Behadur efficiency is optimal for G^2
- Approximation for finite N :
 - One positive outlier --> positive λ is optimal
 - Several deviations of same size --> $\lambda = 0$ is optimal
 - One negative outlier --> negative λ is optimal
- Conclusions:
 - Effect of λ on power is small for $-2 < \lambda < 2$.
 - G^2 appears to be a good default option

2) τ_k Optimization

- Power of G^2 as a function of τ_1 for the storage retrieval model, given $\alpha = .10$ (top), $.05$ (middle) and $.01$ (bottom).
- $c = r = .50, u = .40, a = .60$
- $N = 480$
- Conclusions:
 - Strong effect of τ_1 !!
 - Max. power for $\tau_1 = .652$
 - Thus, $\tau_1 = \dots = \tau_K$ may be a bad default option!



3) θ Optimization

- Model parameters can be divided in H_0 -relevant and H_0 -irrelevant parameters. For the storage-retrieval model test:
 - u and a are H_0 relevant
 - c and r are H_0 irrelevant
- Problem:

How to choose the values of the H_0 -irrelevant parameters so as to maximize the power of the model test?

Approximate power of the G^2 test for the storage-retrieval model ($\alpha = .05, N_1 = 320, N_2 = 160$)

Parameter values under H_1				ncp	approx
c	r	u	a	$\gamma_{(0)}$	$1-\beta(\pi)$
.10	.80	.40	.60	12.49	.94
.10	.20	.40	.60	12.49	.94
.50	.80	.40	.60	8.92	.85
.50	.20	.40	.60	8.92	.85
.90	.80	.40	.60	2.53	.36
.90	.20	.40	.60	2.53	.36

4) Conditional versus unconditional tests

- Consider two nested models:

- M_0 with parameter space Ω_0
- M_1 with parameter space Ω_1
- $\Omega_1 \subset \Omega_0$

- Problem:

M_1 can be tested by an unconditional or a conditional G^2 test provided that M_0 holds.
Which test is more powerful?

Example: Storage-retrieval model

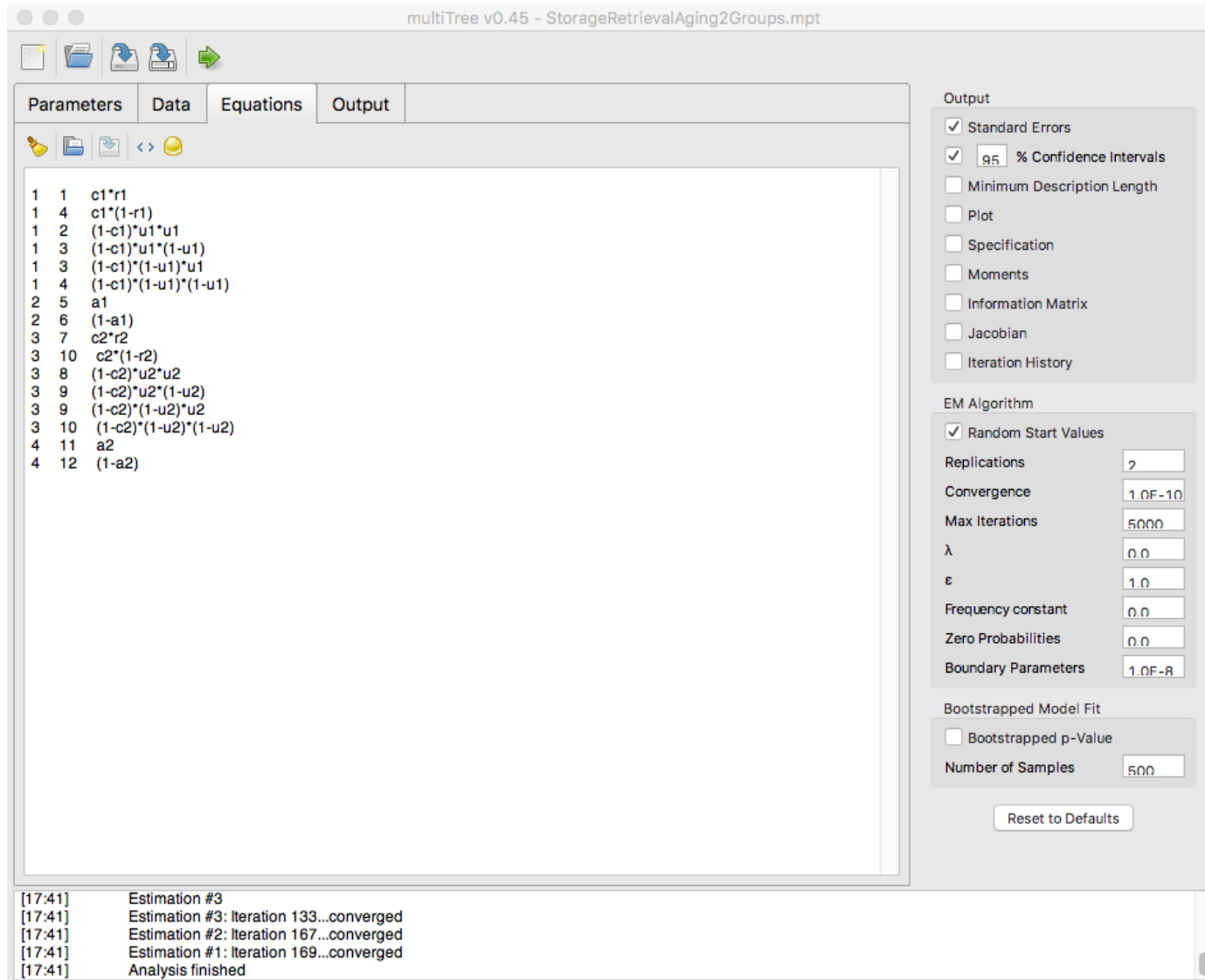
- $N_1 = 160, N_2 = 80$
- $M_0: u = a$
- $M_1: u = a$ and $c = .30$
- Under $H_1: c = r = u = a = .50$ we obtain ($\alpha = .05$):
 - $G^2(M_1)$: $df = 4-2 = 2, \gamma_{(0)} = 8.62, 1-\beta(\pi) = .75$
 - $G^2(M_1)-G^2(M_0)$: $df = 2-1 = 1, \gamma_{(0)} = 8.62, 1-\beta(\pi) = .85$
- Therefore, use conditional G^2 difference tests whenever possible.

Summary and conclusions

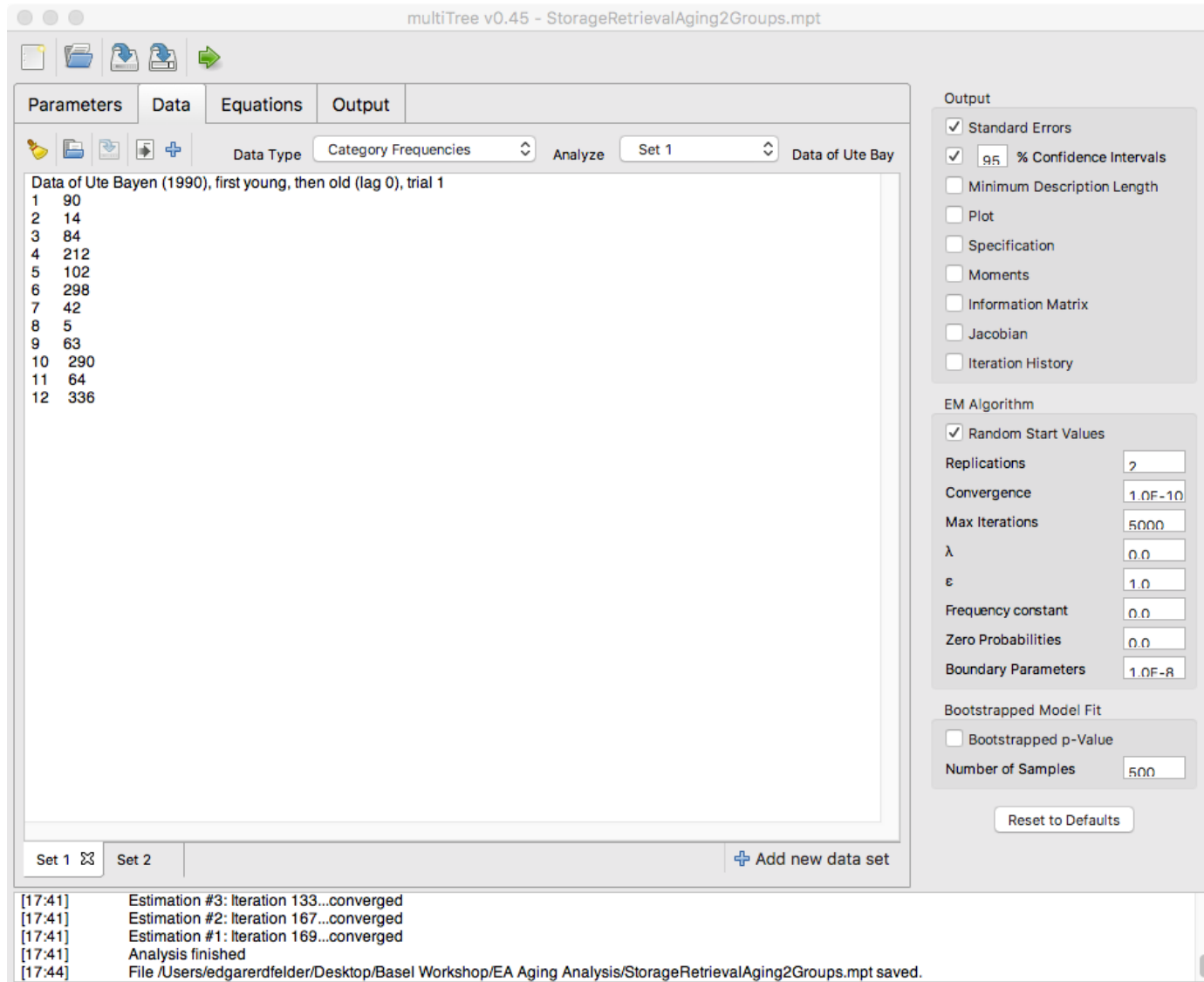
- Do not ignore the power of model tests!
- The proposed approximation method works very well for joint PMMs with typical sample sizes
- Choose same λ in the PD^λ statistic and noncentrality parameter $\gamma(\lambda)$
- G^2 is a good default option for several reasons:
 - Approximation accuracy is optimal
 - Maximum power for “diffuse” noncentrality structures
 - Option of conditional tests
- Do not forget to optimize context conditions:
 - τ_k optimization
 - θ optimization
 - conditional tests whenever possible.

5) Power analyses using multiTree

Example: Age group comparison



Example: Age group comparison



Definition of baseline model

multiTree v0.45 - StorageRetrievalAging2Groups.mpt

Parameters Data Equations Output

Hierarchical Model Families

☒ Define current model as new baseline model (needs to be estimated before it can serve as a baseline).

☐ Compare current model against baseline model

a1	= u1	0.25431
a2	= u2	0.15795
c1	free	0.44815
c2	free	0.41565
r1	free	0.50205
r2	free	0.25265
u1	free	0.25431
u2	free	0.15795

Specification

Number of trees	4
Number of categories	12
Number of free categories	8
Number of parameters	8
Number of constrained parameters	2
Degrees of freedom	2

Output

☒ Standard Errors

☒ 95 % Confidence Intervals

☐ Minimum Description Length

☐ Plot

☐ Specification

☐ Moments

☐ Information Matrix

☐ Jacobian

☐ Iteration History

EM Algorithm

☒ Random Start Values

Replications 2

Convergence 1.0E-10

Max Iterations 5000

λ 0.0

ϵ 1.0

Frequency constant 0.0

Zero Probabilities 0.0

Boundary Parameters 1.0E-8

Bootstrapped Model Fit

☐ Bootstrapped p-Value

Number of Samples 500

Reset to Defaults

[17:48] Estimation #2
[17:48] Estimation #1: Iteration 158...converged
[17:48] Estimation #3: Iteration 164...converged
[17:48] Estimation #2: Iteration 197...converged
[17:48] Analysis finished

H_0 : No age differences in retrieval

multiTree v0.45 - StorageRetrievalAging2Groups.mpt

Parameters Data Equations Output

Hierarchical Model Families

☐ Define current model as new baseline model (needs to be estimated before it can serve as a baseline).

☒ Compare current model against baseline model

a1	= u1	0.2600F
a2	= u2	0.1354F
c1	free	0.4714F
c2	free	0.2359F
r1	free	0.4664F
r2	= r1	0.4664F
u1	free	0.2600F
u2	free	0.1354F

Specification

Number of trees	4
Number of categories	12
Number of free categories	8
Number of parameters	8
Number of constrained parameters	3
Degrees of freedom	3

Output

☒ Standard Errors

☒ 95 % Confidence Intervals

☐ Minimum Description Length

☐ Plot

☐ Specification

☐ Moments

☐ Information Matrix

☐ Jacobian

☐ Iteration History

EM Algorithm

☒ Random Start Values

Replications 2

Convergence 1.0E-10

Max Iterations 5000

λ 0.0

ϵ 1.0

Frequency constant 0.0

Zero Probabilities 0.0

Boundary Parameters 1.0E-8

Bootstrapped Model Fit

☐ Bootstrapped p-Value

Number of Samples 500

Reset to Defaults

[17:37] Estimation #3
[17:37] Estimation #2: Iteration 116...converged
[17:37] Estimation #1: Iteration 139...converged
[17:37] Estimation #3: Iteration 140...converged
[17:37] Analysis finished

Is insignificant outcome due to lack of power?

multiTree v0.45 - StorageRetrievalAging2Groups.mpt

Parameters Data Equations Output

Model Fit

PD^{lambda}=0.0 (df=3) = 3.92165 p = 0.27005

ln(likelihood) = -1178.07830
 AIC = 2366.15661
 BIC = 2393.04540
 Delta AIC = -2.07835
 Delta BIC = -18.21163

Difference to Baseline Model

PD^{lambda}=0.0 (df=1) = 3.76626 p = 0.05230

AIC difference = 1.76626
 BIC difference = -3.61150
 Ratio of AIC weights = 0.29253
 Ratio of BIC weights = 0.85885

	Baseline	Current
a1	= u1	= u1
a2	= u2	= u2
c1	free	free
c2	free	free

Output

☒ Standard Errors
☒ 95 % Confidence Intervals
☐ Minimum Description Length
☐ Plot
☐ Specification
☐ Moments
☐ Information Matrix
☐ Jacobian
☐ Iteration History

EM Algorithm

☒ Random Start Values
 Replications: 2
 Convergence: 1.0E-10
 Max Iterations: 5000
 λ: 0.0
 ε: 1.0
 Frequency constant: 0.0
 Zero Probabilities: 0.0
 Boundary Parameters: 1.0E-8

Bootstrapped Model Fit

☐ Bootstrapped p-Value
 Number of Samples: 500

Reset to Defaults

[17:37] Estimation #3
 [17:37] Estimation #2: Iteration 116...converged
 [17:37] Estimation #1: Iteration 139...converged
 [17:37] Estimation #3: Iteration 140...converged
 [17:37] Analysis finished

multiTree power analysis window

Power Analysis

Statistical power of a test is defined as the probability of rejecting a null hypothesis if it is in fact false, and depends on the alpha error, effect size, and sample size. To perform a power analysis, 'true' population values of the parameters, a H1 model and a H0 model need to be specified. The H1 model is usually chosen such that it yields a perfect fit to the data. The H0 model represents a more restrictive hierarchically nested model. The additional constraints inherent in the H0 model compared to those of the H1 model finally define the particular null hypothesis of interest. That is, the calculated power expresses the probability to reject this additional constraint if it is in fact false.

Type of power analysis

☒ A-priori: Compute required sample size given power, alpha, and effect size.

☐ Post-hoc: Compute achieved power given sample size, alpha, and effect size.

Alpha error probability: 0.05

Desired power (ignored in post-hoc power analysis): 0.95

Please specify the parameter values in the population as well as the H1 and the H0 model:

c1	0.44813	free	0.44813	free	0.44813
c2	0.41563	free	0.41563	free	0.41563
r1	0.50209	free	0.50209	free	0.50209
r2	0.25263	free	0.25263	= r1	0.25263

Please enter the number of observations (represent weights in a-priori power analysis)

Tree: 1 400.0

Tree: 2 400.0

Tree: 3 400.0

OK Cancel

multiTree power analysis output

multiTree v0.45 - StorageRetrievalAging2GroupsPowerBeispiel.mpt

Parameters Data Equations Output

	Population	H1	H0
a1	= 0.25431	= u1	= u1
a2	= 0.15793	= u2	= u2
c1	= 0.44813	free	free
c2	= 0.41563	free	free
r1	= 0.50209	free	free
r2	= 0.25263	free	= r1
u1	= 0.25431	free	free
u2	= 0.15793	free	free

Required number of observations = 5613.62096
 Required observations per tree:
 Tree: 1 = 1403.40524
 Tree: 2 = 1403.40524
 Tree: 3 = 1403.40524
 Tree: 4 = 1403.40524

Model Fit
 H0 Model $PD^{\lambda=0.0}$ (df=3) = 13.21474
 H1 Model $PD^{\lambda=0.0}$ (df=2) = 0.00000

Effect size w = 0.04852
 Non-centrality parameter = 13.21474
 Critical Chi-square = 3.84146
 Delta df = 1

Output

☒ Standard Errors
☒ 95 % Confidence Intervals
☐ Minimum Description Length
☐ Plot
☐ Specification
☐ Moments
☐ Information Matrix
☐ Jacobian
☐ Iteration History

EM Algorithm

☒ Random Start Values
 Replications = 2
 Convergence = 1.0E-10
 Max Iterations = 5000
 λ = 0.0
 ϵ = 1.0
 Frequency constant = 0.0
 Zero Probabilities = 0.0
 Boundary Parameters = 1.0E-8

Bootstrapped Model Fit

☐ Bootstrapped p-Value
 Number of Samples = 500

Reset to Defaults

[14:28] Running power analysis... target ncp = 12.9947 current ncp = 1.73102
 [14:28] Running power analysis... target ncp = 12.9947 current ncp = 3.68079
 [14:28] Running power analysis... target ncp = 12.9947 current ncp = 7.10904
 [14:28] Running power analysis... target ncp = 12.9947 current ncp = 11.29318
 [14:28] Power analysis finished.

4.3) Model selection

An implementation of the MDL principle was provided by [Rissanen \(2001\)](#) who derived the normalized maximum likelihood (NML) to measure the stochastic complexity of a model given a data set,

$$\text{NML} = -\text{LML} + C_{\text{NML}}(N), \quad (1)$$

where the maximum log-likelihood (LML) as a measure of fit is weighted against the complexity term

$$C_{\text{NML}}(N) = \ln \int_{\mathcal{X}^N} f(\mathbf{x}|\hat{\boldsymbol{\theta}}(\mathbf{x})) d\mathbf{x}. \quad (2)$$

This complexity term is the natural logarithm of the integral over the maximum likelihoods across the whole outcome space \mathcal{X}^N of potentially observable vectors \mathbf{x} with N observations. Accordingly, a complex model that fits a wide range of observable data vectors will have a large value of $C_{\text{NML}}(N)$ compared to a model that fits only a small subset of observable data ([Myung, Navarro, & Pitt, 2006](#)). Unfortunately, there is no general closed-form expression of $C_{\text{NML}}(N)$ and numerical estimation techniques such as Monte Carlo (MC) integration are often too time intensive for practical purposes. An alternative is the Fisher information approximation (FIA; [Rissanen, 1996](#)),

$$\text{FIA} = -\text{LML} + C_{\text{FIA}}(N), \quad (3)$$

which is asymptotically equivalent to NML. The complexity term $C_{\text{FIA}}(N)$ covers the number of free parameters S and the number of observations N in the first summand and considers the functional form of the model in the second,

$$C_{\text{FIA}}(N) = \frac{S}{2} \ln \left(\frac{N}{2\pi} \right) + \ln \int_{\Omega} \sqrt{|\mathbf{I}(\boldsymbol{\theta})|} d\boldsymbol{\theta}, \quad (4)$$

where $\mathbf{I}(\boldsymbol{\theta})$ is the Fisher information matrix of sample size one. This

Heck, Moshagen & Erdfelder (2014)

To avoid biases in model selection using FIA for NML stable models, we propose to check whether the $C_{\text{FIA}}(N)$ rank order of the candidate models is invariant across different numbers N of observations. Based on the definition of FIA in (4) it is easy to show that for any two models with a fixed but unequal number of parameters S_i and S_j , respectively, the $C_{\text{FIA}}(N)$ rank order cannot be identical for all possible sample sizes. Since the integral in (4) is independent of N , it is straightforward to determine the (single) sample size $N'_{i,j}$ for which the complexity terms of two models with $S_i \neq S_j$ are equal. Equating the FIA terms of two models i and j and solving for N yields

$$N'_{i,j} = 2\pi \exp \left[\frac{2}{S_i - S_j} \left(\ln \int_{\Omega_j} \sqrt{|\mathbf{I}_j(\boldsymbol{\theta})|} d\boldsymbol{\theta} - \ln \int_{\Omega_i} \sqrt{|\mathbf{I}_i(\boldsymbol{\theta})|} d\boldsymbol{\theta} \right) \right]. \quad (5)$$

When $N > N'_{i,j}$, the $C_{\text{FIA}}(N)$ terms of the two competing models i and j will always result in the same rank order. Because $C_{\text{FIA}}(N)$ approximates $C_{\text{NML}}(N)$ for increasing N , this must be the correct (i.e., NML-consistent) rank order. By implication, for any $N < N'_{i,j}$ the rank order of complexity terms is incorrectly inverted.

Heck, Moshagen & Erdfelder (2014)

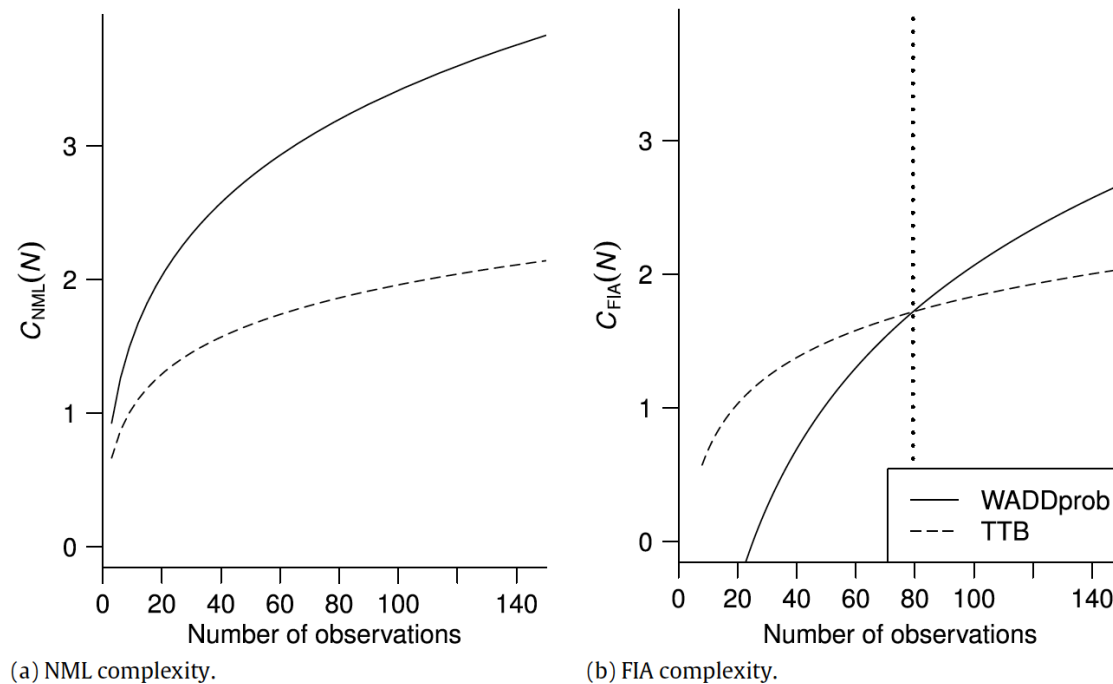


Fig. 1. NML and FIA complexities for two decision strategies, take-the-best (TTB) and a probabilistic weighted-additive rule (WADDprob; Fig. 4), as functions of the number of observations N . The dotted vertical line for FIA marks the lower bound $N' = 80$.